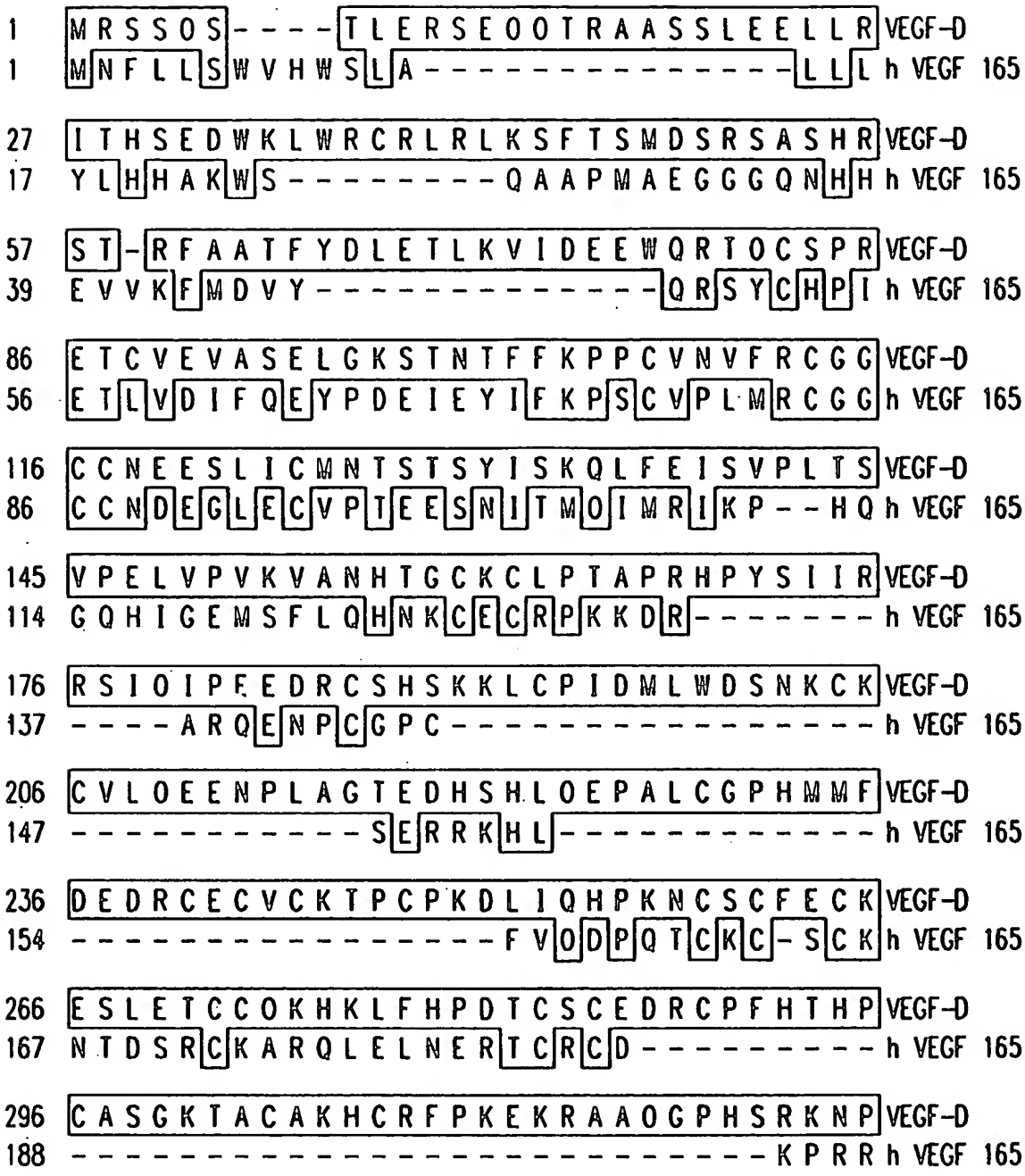
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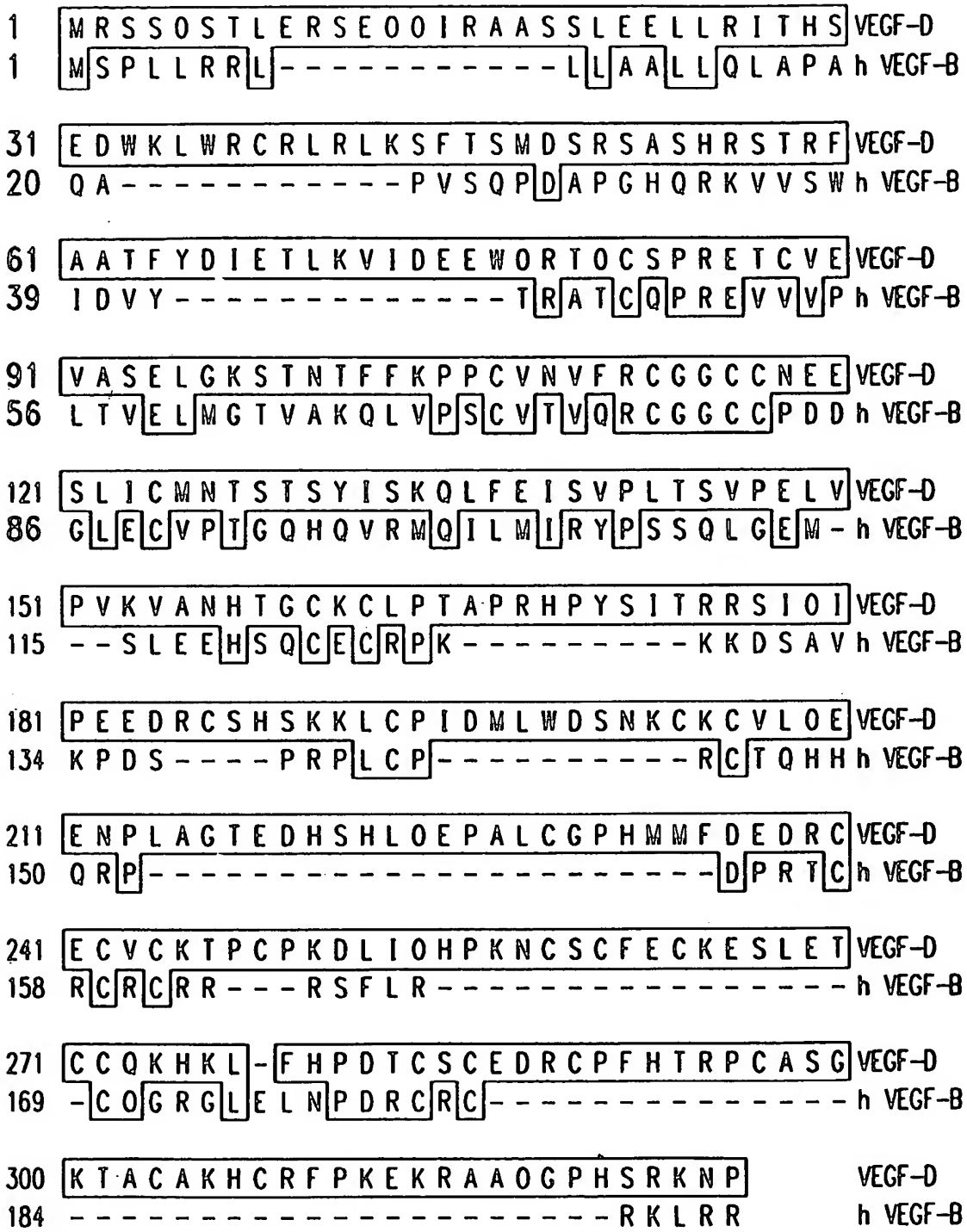
1 MNFLLSWVHWSLA--------------LLL h VEGF 165
27 ITHSEDWKLWRCRLRLKSFTSMDSRSASHR VEGF-D
17 YLHHAKWS---------QAAPMAEGGGQNHH h VEGF 165
57 ST-RFAATFYDLETLKVIDEEWQRTQCSPR VEGF-D
39 EVVKFMDVY-----------QRSYCHPI h VEGF 165
86 ETCVEVASELGKSTNTFFKPPCVNVFRCGG VEGF-D
56 ETLVDIFQEYPDEIEYIFKPSCVPLMRCGG h VEGF 165
116 CCNEESLICMNTSTSYISKQLFEISVPLTS VEGF-D
86 CCNDEGLECVPTEESNITMQIMRIKP--HQ h VEGF 165
145 VPELVPVKVANHTGCKCLPTAPRHPYSIIR VEGF-D
114 GQHIGEMSFLQHNKCECRPKKDR-------- h VEGF 165
176 RSIQIPFEDRCSHSKKLCPIDMLWDSNKCK VEGF-D
137 ----ARQENPCGPC----------------- h VEGF 165
206 CVLQEENPLAGTEDHSHLQEPALCGPHMMF VEGF-D
147 ----------SERRKHL------------- h VEGF 165
236 DEDRCECVCKTPCPKDLIQHPKNCSCFECK VEGF-D
154 ----------------FVQDPQTCKC-SCK h VEGF 165
266 ESLETCCQKHKLFHPDTCSCEDRCPFHTHP VEGF-D
167 NTDSRCKARQLELNERTCRCD---------- h VEGF 165
296 CASGKTACAKHCRFPKEKRAAQGPHSRKNP VEGF-D
188 ----------------------------KPRR h VEGF 165

FIG. 1A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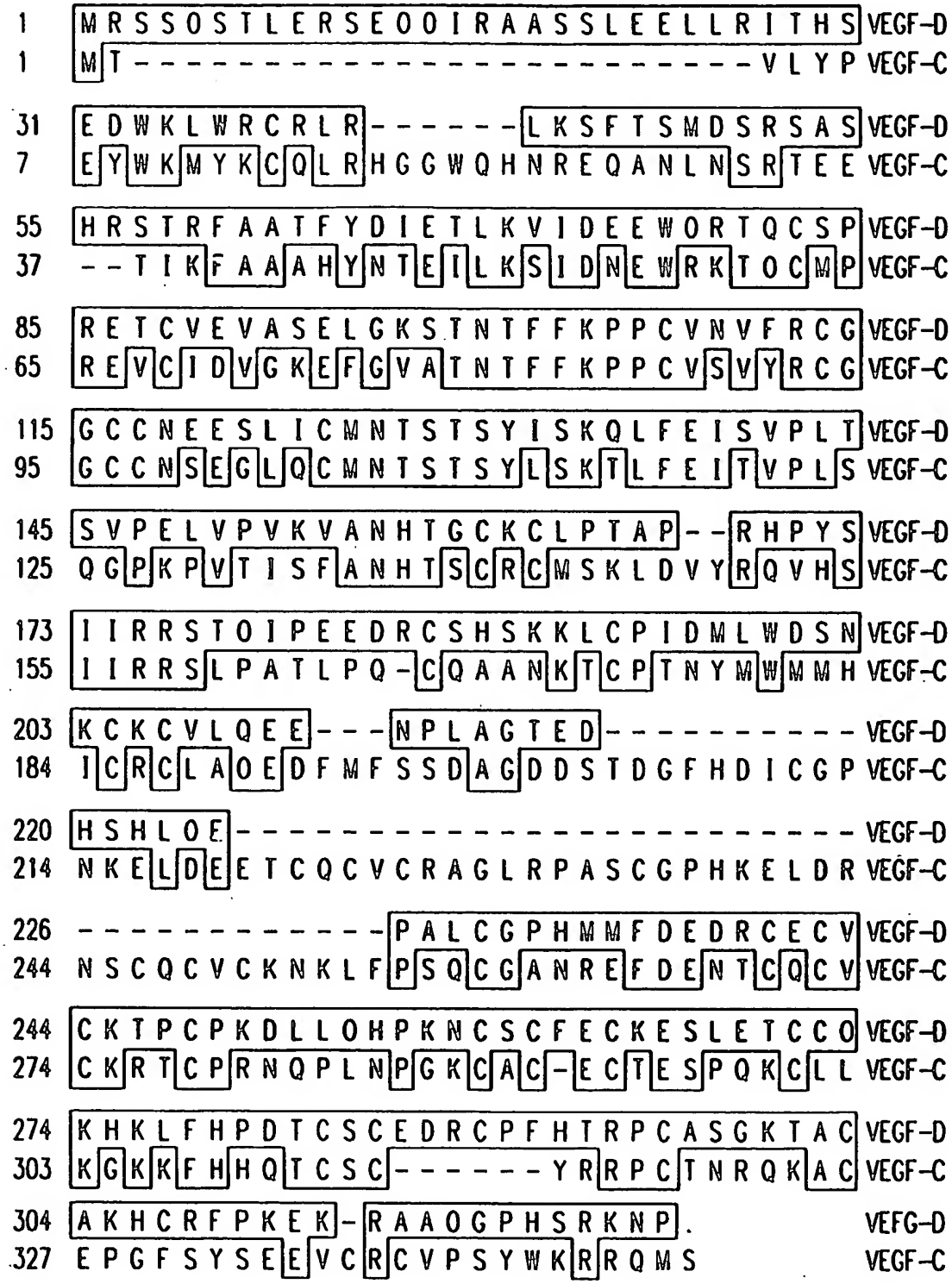
1 MSPLLRRL----------LLAALLQLAPA h VEGF-B
31 EDWKLWRCRLRLKSFTSMDSRSASHRSTRF VEGF-D
20 QA----------PVSQPDAPGHQRKVVSW h VEGF-B
61 AATFYDIETLKVIDEEWQRTQCSPRETCVE VEGF-D
39 IDVY----------TRATCQPREVVVP h VEGF-B
91 VASELGKSTNTFFKPPCVNVFRCGGCCNEE VEGF-D
56 LTVELMGTVAKQLVPSCVTVQRCGGCCPDD h VEGF-B
121 SLICMNTSTSYISKQLFEISVPLTSVPELV VEGF-D
86 GLECVPTGQHQVRMQILMIRYPSSQLGEM- h VEGF-B
151 PVKVANHTGCKCLPTAPRHPYSITRRSIQI VEGF-D
115 --SLEEHSQCECRPK----------KKDSAV h VEGF-B
181 PEEDRCSHSKKLCPIDMLWDSNKCKCVLQE VEGF-D
134 KPDS----PRPLCP----------RCTQHH h VEGF-B
211 ENPLAGTEDHSHLQEPALCGPHMMFDEDRC VEGF-D
150 QRP----------D PRTC h VEGF-B
241 ECVCKTPCPKDLIQHPKNCSCFECKESLET VEGF-D
158 RCRCRR---RSFLR----------h VEGF-B
271 CCQKHKL-FHPDTCSCEDRCPFHTRPCASG VEGF-D
169 -CQGRGLELNPDRCRC----------h VEGF-B
300 KTACAKHCRFPKEKRAAQGPHSRKNP VEGF-D
184 ----------RKLRR h VEGF-B

FIG. 1B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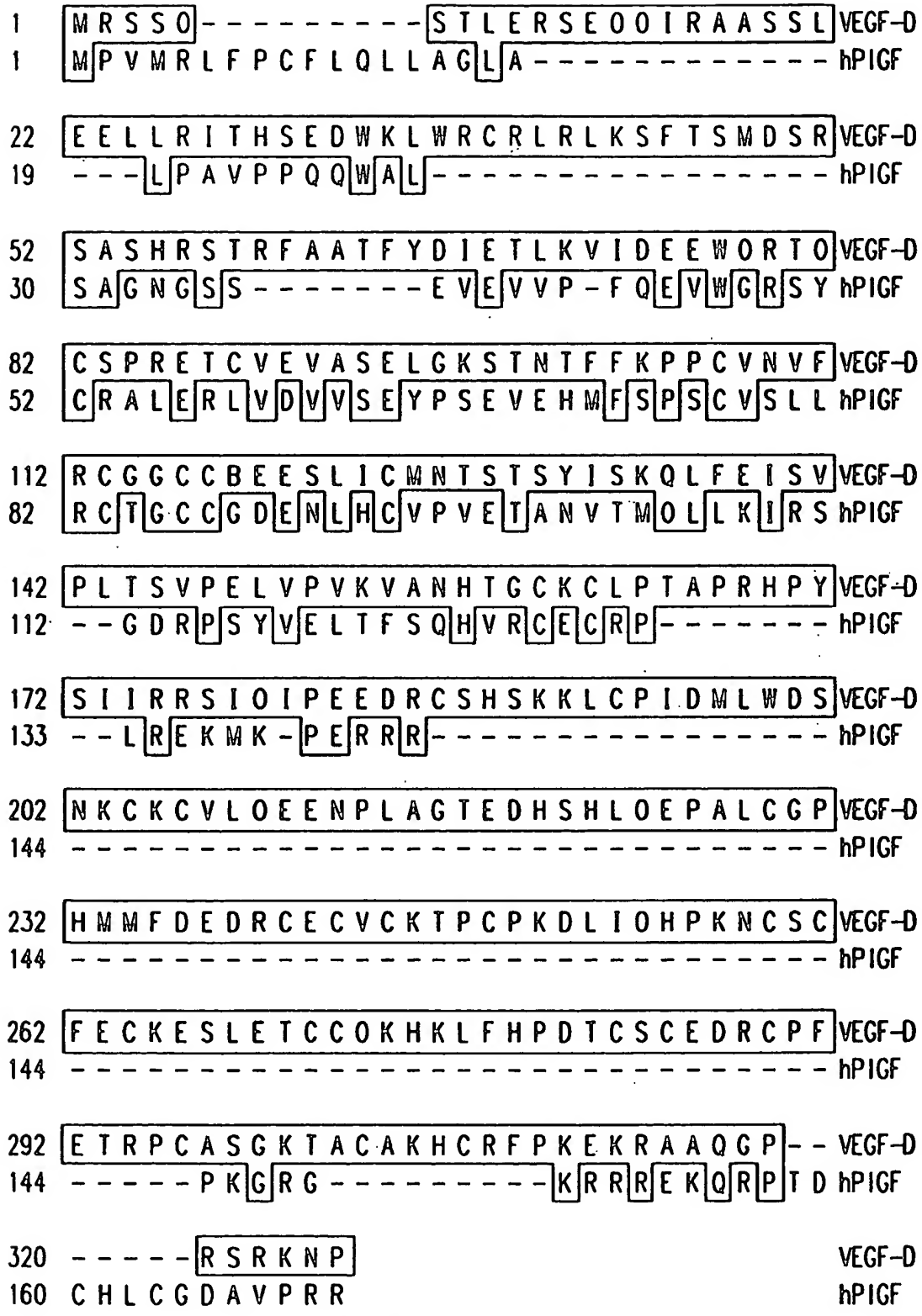
1 MT----------VLYP VEGF-C
31 EDWKLWRCRLR------LKSFTSMDSRSAS VEGF-D
7 EYWKMYKCQLRHGGWQHNREQANLNSRTEE VEGF-C
55 HRSTRFAATFYDIETLKVIDEEWQRTQCSP VEGF-D
37 --TIKFAAAHYNTEILKSIDNEWRKTQCMP VEGF-C
85 RETCVEVASELGKSTNTFFKPPCVNVFRCG VEGF-D
65 REVCIDVGKEFGVATNTFFKPPCVSVYRCG VEGF-C
115 GCCNEESLICMNTSTSYISKQLFEISVPLT VEGF-D
95 GCCNSEGLQCMNTSTSYLSKTLFEITVPLS VEGF-C
145 SVPELVPVKVANHTGCKCLPTAP--RHPYS VEGF-D
125 QGPKPVTISFANHTSCRCMSKLDVYRQVHS VEGF-C
173 IIRRSTQIPEEDRCSHSKKLCPIDMLWDSN VEGF-D
155 IIRRSLPATLPQ-CQAANKTCPTNYMWMMH VEGF-C
203 KCKCVLQEE---NPLAGTED---------- VEGF-D
184 ICRCLAQEDFMFSSDAGDDSTDGFHDICGP VEGF-C
220 HSHLQE---------- VEGF-D
214 NKELDEETCQCVCRAGLRPASCGPHKELDR VEGF-C
226 ----------PALCGPHMMFDEDRCECV VEGF-D
244 NSCQCVCKNKLFPSQCGANREFDENTCQCV VEGF-C
244 CKTPCPKDLLQHPKNCSCFECKESLETCCQ VEGF-D
274 CKRTCPRNQPLNPGKCAC-ECTESPQKCLL VEGF-C
274 KHKLFHPDTCSCEDRCPFHTRPCASGKTAC VEGF-D
303 KGKKFHHQTCSC------YRRPCTNRQKAC VEGF-C
304 AKHCRFPKEK-RAAQGPHSRKNP. VEFG-D
327 EPGFSYSEEVCRCVPSYWKRRQMS VEGF-C

FIG. 1C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1 MPVMRLFPCFLQLLAGLA---------- hPlGF
22 EELLRITHSEDWKLWRCRLRLKSFTSMDSR VEGF-D
19 ---LPAVPPQQWALL---------- hPlGF
52 SASHRSTRFAATFYDIETLKVIDEEWQRTQ VEGF-D
30 SAGNGSS-------EVEVVP-FQEVWGRSY hPlGF
82 CSPRETCVEVASELGKSTNTFFKPPCVNVF VEGF-D
52 CRALERLVDVVSEYPSEVEHMFSPSCVSLL hPlGF
112 RCGGCCBEESLICMNTSTSYISKQLFEISV VEGF-D
82 RCTGCCGDENLHCVPVETANVTMQLLKIRS hPlGF
142 PLTSVPELVPVKVANHTGCKCLPTAPRHPY VEGF-D
112 --GDRPSYVELTFSQHVRCECRP------- hPlGF
172 SIIRRSIQIPEEDRCSHSKKLCPIDMLWDS VEGF-D
133 --LREKMK-PERRR---------- hPlGF
202 NKCKCVLQEENPLAGTEDHSHLQEPALCGP VEGF-D
144 ---------- hPlGF
232 HMMFDEDRCECVCKTPCPKDLIQHPKNCSC VEGF-D
144 ---------- hPlGF
262 FECKESLETCCQKHKLFHPDTCSCEDRCPF VEGF-D
144 ---------- hPlGF
292 ETRPCASGKTACAKHCRFPKEKRAAQGP-- VEGF-D
144 -----PKGRG---------KRRRRKQRPTD hPlGF
320 -----RSRKNP VEGF-D
160 CHLCGDAVPRR hPlGF

FIG. 1D

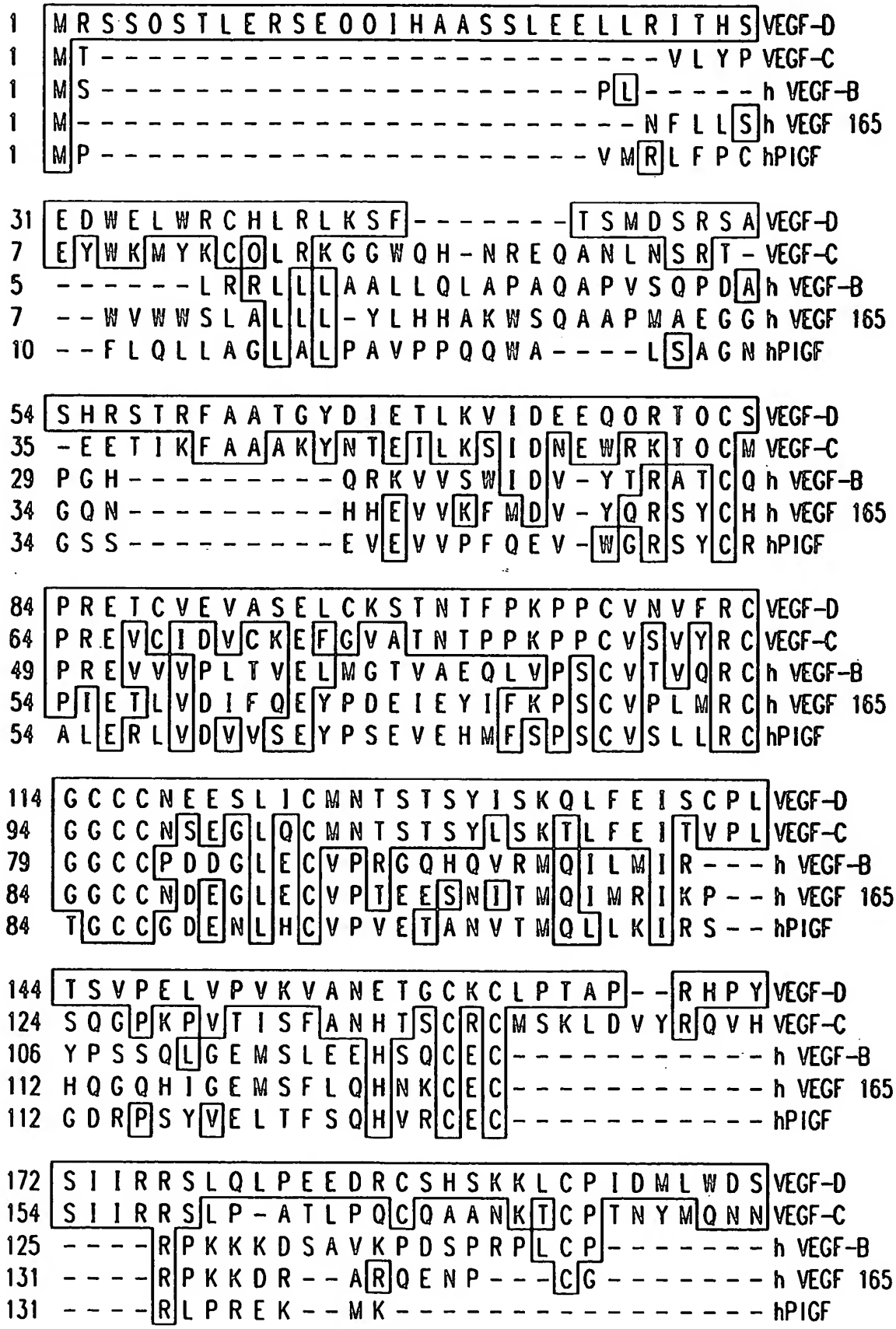
1 MRSSQSTLERSEQQIHAASSLEELLRITHS VEGF-D
1 MT-----------------------VLYP VEGF-C
1 MS----------------------PL-----h VEGF-B
1 M-----------------------NFLLSh VEGF 165
1 MP----------------------VMRLFPC hPIGF
31 EDWELWRCHLRLKSF-------TSMDSRSA VEGF-D
7 EYWKMYKCQLRKGGWQH-NREQANLNSRT- VEGF-C
5 -------LRRLLLAALLQLAPAQAPVSQPDA h VEGF-B
7 --WVWWSLALLL-YLHHAKWSQAAPMAEGG h VEGF 165
10 --FLQLLAGLALPAVPPQQWA----LSAGN hPIGF
54 SHRSTRFAATGYDIETLKVIDEEQQRTQCS VEGF-D
35 -EETIKFAAAKYNTEILKSIDNEWRKTQCM VEGF-C
29 PGH----------QRKVVSWIDV-YTRATCQ h VEGF-B
34 GQN----------HHEVVKFMDV-YQRSYCH h VEGF 165
34 GSS----------EVEVVPFQEV-WGRSYCR hPIGF
84 PRETCVEVASELCKSTNTFPKPPCVNVFRC VEGF-D
64 PREVCIDVCKEFGVATNTPPKPPCVSVYRC VEGF-C
49 PREVVVPLTVELMGTVAEQLVPSCVTVQRC h VEGF-B
54 PIETLVDIFQEYPDEIEYIFKPSCVPLMRC h VEGF 165
54 ALERLVDVVSEYPSEVEHMFSPSCVSLLRC hPIGF
114 GCCCNEESLICMNTSTSYISKQLFEISCPL VEGF-D
94 GGCCNSEGLQCMNTSTSYLSKTLFEITVPL VEGF-C
79 GGCCPDDGLECVPRGQHQVRMQILMIR--- h VEGF-B
84 GGCCNDEGLECVPTEESNITMQIMRIKP-- h VEGF 165
84 TGCCGDENLHCVPVETANVTMQLLKIRS-- hPIGF
144 TSVPELVPVKVANETGCKCLPTAP--RHPY VEGF-D
124 SQGPKPVTISFANHTSCRCMSKLDVYRQVH VEGF-C
106 YPSSQLGEMSLEEHSQCEC---------- h VEGF-B
112 HQGQHIGEMSFLQHNKCEC---------- h VEGF 165
112 GDRPSYVELTFSQHVRCEC---------- hPIGF
172 SIIRRSLQLPEEDRCSHSKKLCPIDMLWDS VEGF-D
154 SIIRRSLP-ATLPQCQAANKTCPTNYMQNN VEGF-C
125 ----RPKKKDSAVKPDSPRPLCP-------- h VEGF-B
131 ----RPKKDR--ARQENP---CG-------- h VEGF 165
131 ----RLPREK--MK---------------- hPIGF

FIG. 2A

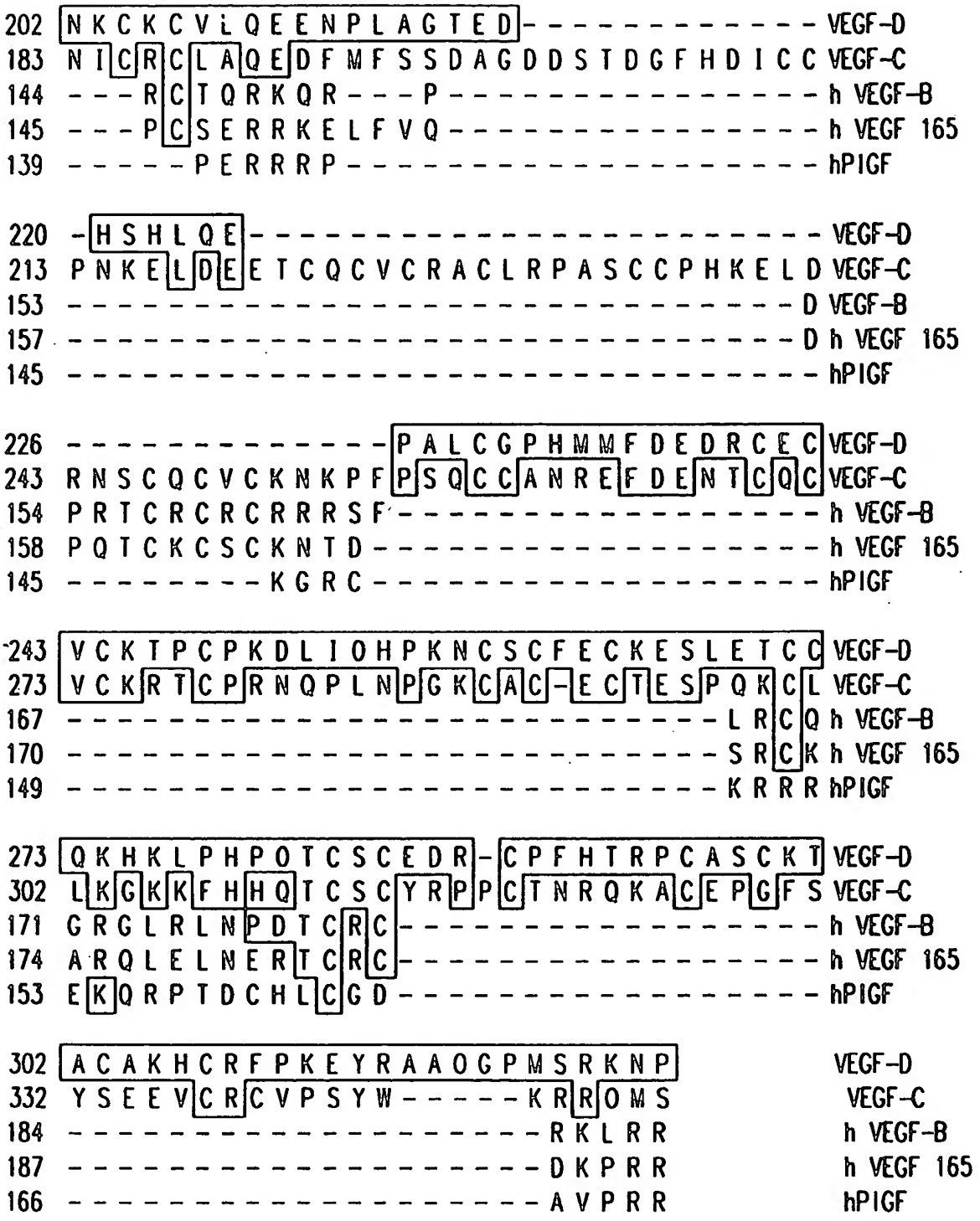
202 NKCKCVLQEENPLAGTED VEGF-D
183 NICRCLAQEDFMFSSDAGDDSTDGFHDICC VEGF-C
144 RCTQRKQRP h VEGF-B
145 PCSERRKELFVQ h VEGF 165
139 PERRRP hPIGF
220 HSHLQE VEGF-D
213 PNKELDEETCQCVCRACLRPASCCPHKELD VEGF-C
153 D VEGF-B
157 D h VEGF 165
145 hPIGF
226 PALCGPHMMFDEDRCECVEGF-D
243 RNSCQCVCKNKPFPSQCCANREFDENTCQCVEGF-C
154 PRTCRCRCRRRSF h VEGF-B
158 PQTCKCSCKNTD h VEGF 165
145 KGRC hPIGF
243 VCKTPCPKDLIQHPKNCSCFECKESLETCC VEGF-D
273 VCKRTCPRNQPLNPGKCACECTESPQKCL VEGF-C
167 LRCQ h VEGF-B
170 SRCK h VEGF 165
149 KRRR hPIGF
273 QKHKLPHPQTCSCEDRCPFHTRPCASCKT VEGF-D
302 LKGKKFHHQTCSCYRPPCTNRQKACEPGFS VEGF-C
171 GRGLRLNPDTCRC h VEGF-B
174 ARQLELNERTCRC h VEGF 165
153 EKQRPTDCHLCGD hPIGF
302 ACAKHCRFPKEYRAAQGPMSRKNP VEGF-D
332 YSEEVCRCVPSYW-----KRROMS VEGF-C
184 RKLRR h VEGF-B
187 DKPRR h VEGF 165
166 AVPRR hPIGF

FIG. 2B

```
          10         20         30         40
MRSSQSTLERSEDDIRAASSLEELLRITHSEDWKLWRCRL

          50         60         70         80
RLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRT

          90         100        110        120
QCSPRETCVEVASELGKSTNTFFKPPCVNVFRCGGCCNEE

         130        140        150        160
SLICMNTSTSYISKQLFEISVPLTSVPELVPVKVANHTGC

         170        180        190        200
KCLPTAPPHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWD

         210        220        230        240
SNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRC

         250        260        270        280
ECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFHP

         290        300        310        320
DTCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPH

SRKNP
```

FIG.3

FIG. 4

GTTGGGTTCCAGCTTTCTGTAGCTGTAAGCATTGGTGGCCACACCACCTCCTTACAA
AGCAACTAGAACCTGCGGCATACATTGGAGAGATTTTTTTAATTTTCTGGACATGAA
GTAAATTTAGAGTGCTTTCTAATTTCAGGTAGAAGACATGTCCACCTTCTGATTATT
TTTGGAGAACATTTTGATTTTTTTCATCTCTCTCTCCCCACCCCTAAGATTGTGCAA
AAAAAGCGTACCTTGCCTAATTGAAATAATTTCATTGGATTTTGATCAGAACTGATT
ATTTGGTTTTCTGTGTGAAGTTTTGAGGTTTCAAACTTTCCTTCTGGAGAATGCCTT
TTGAAACAATTTTCTCTAGCTGCCTGATGTCAACTGCTTAGTAATCAGTGGATATTG
AAATATTCAAAATGTACAGAGAGTGGGTAGTGGTGAATGTTTTCATGATGTTGTACG
TCCAGCTGGTGCAGGGCTCCAGTAATGAACATGGACCAGTGAAGCGATCATCTCAGT
CCACATTGGAACGATCTGAACAGCAGATCAGGGCTGCTTCTAGTTTGGAGGAACTAC
TTCGAATTACTCACTCTGAGGACTGGAAGCTGTGGAGATGCAGGCTGAGGCTCAAAA
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CTTTCTATGACATTGAAACACTAAAAGTTATAGATGAAGAATGGCAAAGAACTCAGT
GCAGCCCTAGAGAAACGTGCGTGGAGGTGGCCAGTGAGCTGGGGAAGAGTACCAACA
CATTCTTCAAGCCCCCTTGTGTGAACGTGTTCCGATGTGGTGGCTGTTGCAATGAAG
AGAGCCTTATCTGTATGAACACCAGCACCTCGTACATTTCCAAACAGCTCTTTGAGA
TATCAGTGCCTTTGACATCAGTACCTGAATTAGTGCCTGTTAAAGTTGCCAATCATA
CAGGTTGTAAGTGCTTGCCAACAGCCCCCCGCCATCCATACTCAATTATCAGAAGAT
CCATCCAGATCCCTGAAGAAGATCGCTGTTCCCATTCCAAGAAACTCTGTCCTATTG
ACATGCTATGGGATAGCAACAAATGTAAATGTGTTTTGCAGGAGGAAAATCCACTTG
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TGTTTGACGAAGATCGTTGCGAGTGTGTCTGTAAAACACCATGTCCCAAAGATCTAA
TCCAGCACCCCAAAAACTGCAGTTGCTTTGAGTGCAAAGAAAGTCTGGAGACCTGCT
GCCAGAAGCACAAGCTATTTCACCCAGACACCTGCAGCTGTGAGGACAGATGCCCCT
TTCATACCAGACCATGTGCAAGTGGCAAAACAGCATGTGCAAAGCATTGCCGCTTTC
CAAAGGAGAAAAGGGCTGCCCAGGGGCCCCACAGCCGAAAGAATCCTTGATTCAGCG
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CACTGTTTTTTTCCCAGGTGTTAAAAAAAAAATCCATTTTACACAGCACCACAGTGA
ATCCAGACCAACCTTCCATTCACACCAGCTAAGGAGTCCCTGGTTCATTGATGGATG
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ATCCTTTTGTTTAGTTTTGTTTTTGTTTTTTGGTGAATGAGAAAGGTGTGCTGGTCA
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HSEDWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPR
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DSNKCKCVLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKTPCPKDLIQHP
KNCSCFECKESLETCCQKHKLFHPDTCSCEDRCPFHTRPCASGKTACAKHCRFPKEK
RAAQGPHSRKNP

FIG. 5

FIG. 6

GGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACAACTGCTTAGTCAT
CGGTAGACATTTAAAATATTCAAAATGTATGGAGAATGGGGAATGGGGAATATCCTC
ATGATGTTCCATGTGTACTTGGTGCAGGGCTTCAGGAGCGAACATGGACCAGTGAAG
GATTTTTCTTTTGAGCGATCATCCCGGTCCATGTTGGAACGATCTGAACAACAGATC
CGAGCAGCTTCTAGTTTGGAGGAGTTGCTGCAAATCGCGCACTCTGAGGACTGGAAG
CTGTGGCGATGCCGGTTGAAGCTCAAAAGTCTTGCCAGTATGGACTCACGCTCAGCA
TCCCATCGCTCCACCAGATTTGCGGCAACTTTCTATGACACTGAAACACTAAAAGTT
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GCCAGTGAGCTGGGGAAGACAACCAACACATTCTTCAAGCCCCCCTGTGTAAATGTC
TTCCGGTGTGGAGGCTGCTGCAACGAAGAGGGTGTGATGTGTATGAACACAAGCACC
TCCTACATCTCCAAACAGCTCTTTGAGATATCAGTGCCTCTGACATCAGTGCCCGAG
TTAGTGCCTGTTAAAATTGCCAACCATACGGGTTGTAAGTGCTTGCCCACGGGCCCC
CGCCATCCTTACTCAATTATCAGAAGATCCATTCAGACCCCAGAAGAAGATGAATGT
CCTCATTCCAAGAAACTCTGTCCTATTGACATGCTGTGGGATAACACCAAATGTAAA
TGTGTTTTGCAAGACGAGACTCCACTGCCTGGGACAGAAGACCACTCTTACCTCCAG
GAACCCACTCTCTGTGGACCGCACATGACGTTTGATGAAGATCGCTGTGAGTGCGTC
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GAGTGCAAAGAAAGTCTGGAGAGCTGCTGCCAAAAGCACAAGATTTTTCACCCAGAC
ACCTGCAGCTGTGAGGACAGATGTCCTTTTCACACCAGAACATGTGCAAGTAGAAAG
CCAGCCTGTGGAAAGCACTGGCGCTTTCCAAAGGAGACAAGGGCCCAGGGACTCTAC
AGCCAGGAGAACCCTTGATTCAACTTCCTTTCAAGTCCCCCCATCTCTGTCATTTTA
AACAGCTCACTGCTTTGTCAAGTTGCTGTCACTGTTGCCCACTACCCCTTGAACATG
TGCAAACACAGACACACACACACACACACACACAGAGCAACTAGAATTATGTTTTCT
AGGTGCTGCCTAAG

FIG. 7

AAACTTTGCTTCTGGAGAATGCCTTTTGCAACACTTTTCAGTAGCTGCCTGGAAACA
ACTGCTTAGTCATCGGTAGACATTTAAAATATTCAAAATGTATGGAGAATGGGGAAT
GGGGAATATCCTCATGATGTTCCATGTGTACTTGGTGCAGGGCTTCAGGAGCGAACA
TGGACCAGTGAAGCGATCATCCCGGTCCATGTTGGAACGATCTGAACAACAGATCCG
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CCATCCTTACTCAATTATCAGAAGATCCATTCAGACCCCAGAAGAAGATGAATGTCC
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ACCCACTCTCTGTGGACCGCACATGACGTTTGATGAAGATCGCTGTGAGTGCGTCTG
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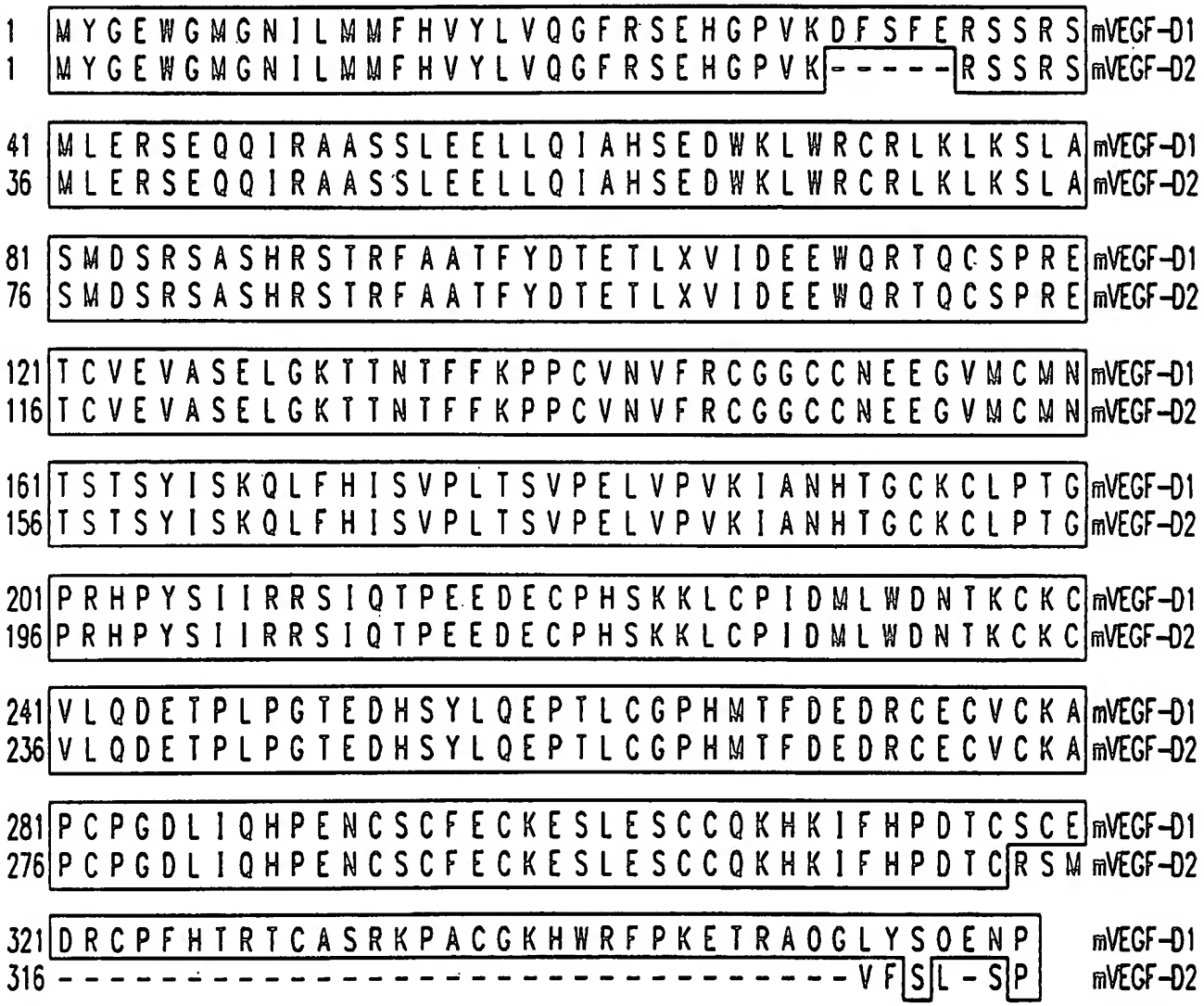
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36 MLERSEQQIRAASSLEELLQIAHSEDWKLWRCRLKLKSLA mVEGF-D2
81 SMDSRSASHRSTRFAATFYDTETLXVIDEEWQRTQCSPRE mVEGF-D1
76 SMDSRSASHRSTRFAATFYDTETLXVIDEEWQRTQCSPRE mVEGF-D2
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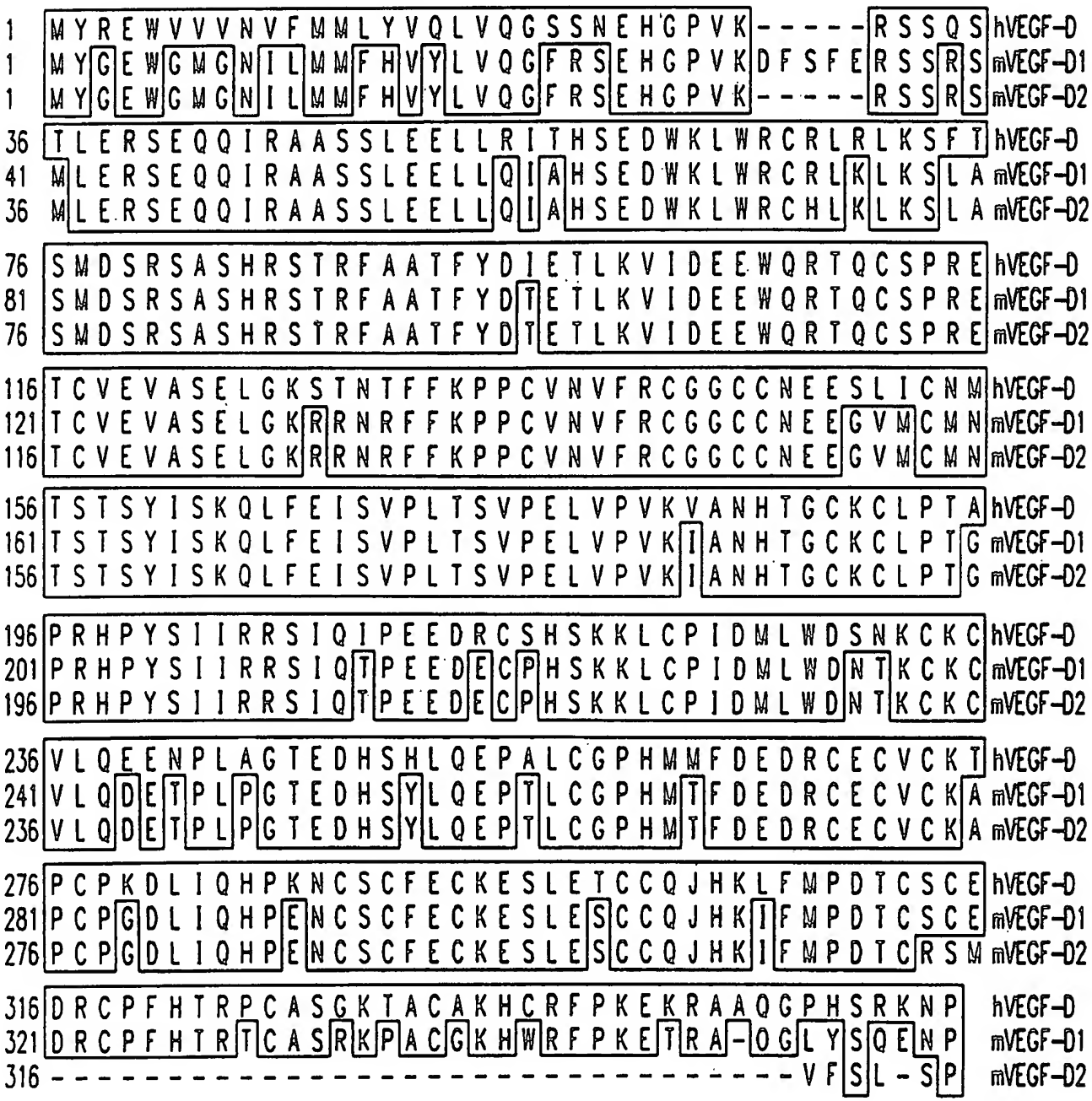
116 TCVEVASELGKTTNTFFKPPCVNVFRCGGCCNEEGVMCMN mVEGF-D2
161 TSTSYISKQLFHISVPLTSVPELVPVKIANHTGCKCLPTG mVEGF-D1
156 TSTSYISKQLFHISVPLTSVPELVPVKIANHTGCKCLPTG mVEGF-D2
201 PRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC mVEGF-D1
196 PRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC mVEGF-D2
241 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKA mVEGF-D1
236 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKA mVEGF-D2
281 PCPGDLIQHPENCSCFECKESLESCCQKHKIFHPDTCSCE mVEGF-D1
276 PCPGDLIQHPENCSCFECKESLESCCQKHKIFHPDTCRSM mVEGF-D2
321 DRCPFHTRTCASRKPACGKHWRFPKETRAQGLYSQENP mVEGF-D1
316 ----------VFSL-SP mVEGF-D2

FIG.8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41 MLERSEQQIRAASSLEELLQIAHSEDWKLWRCRLKLKSLA mVEGF-D1
36 MLERSEQQIRAASSLEELLQIAHSEDWKLWRCHLKLKSLA mVEGF-D2
76 SMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQCSPRE hVEGF-D
81 SMDSRSASHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE mVEGF-D1
76 SMDSRSASHRSTRFAATFYDTETLKVIDEEWQRTQCSPRE mVEGF-D2
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121 TCVEVASELGKRRNRFFKPPCVNVFRCGGCCNEEGVMCMN mVEGF-D1
116 TCVEVASELGKRRNRFFKPPCVNVFRCGGCCNEEGVMCMN mVEGF-D2
156 TSTSYISKQLFEISVPLTSVPELVPVKVANHTGCKCLPTA hVEGF-D
161 TSTSYISKQLFEISVPLTSVPELVPVKIANHTGCKCLPTG mVEGF-D1
156 TSTSYISKQLFEISVPLTSVPELVPVKIANHTGCKCLPTG mVEGF-D2
196 PRHPYSIIRRSIQIPEEDRCSHSKKLCPIDMLWDSNKCKC hVEGF-D
201 PRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC mVEGF-D1
196 PRHPYSIIRRSIQTPEEDECPHSKKLCPIDMLWDNTKCKC mVEGF-D2
236 VLQEENPLAGTEDHSHLQEPALCGPHMMFDEDRCECVCKT hVEGF-D
241 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKA mVEGF-D1
236 VLQDETPLPGTEDHSYLQEPTLCGPHMTFDEDRCECVCKA mVEGF-D2
276 PCPKDLIQHPKNCSCFECKESLETCCQJHKLFMPDTCSCE hVEGF-D
281 PCPGDLIQHPENCSCFECKESLESCCQJHKIFMPDTCSCE mVEGF-D1
276 PCPGDLIQHPENCSCFECKESLESCCQJHKIFMPDTCRSM mVEGF-D2
316 DRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP hVEGF-D
321 DRCPFHTRTCASRKPACGKHWRFPKETRA-QGLYSQENP mVEGF-D1
316 ----------VFSL-SP mVEGF-D2

FIG.9

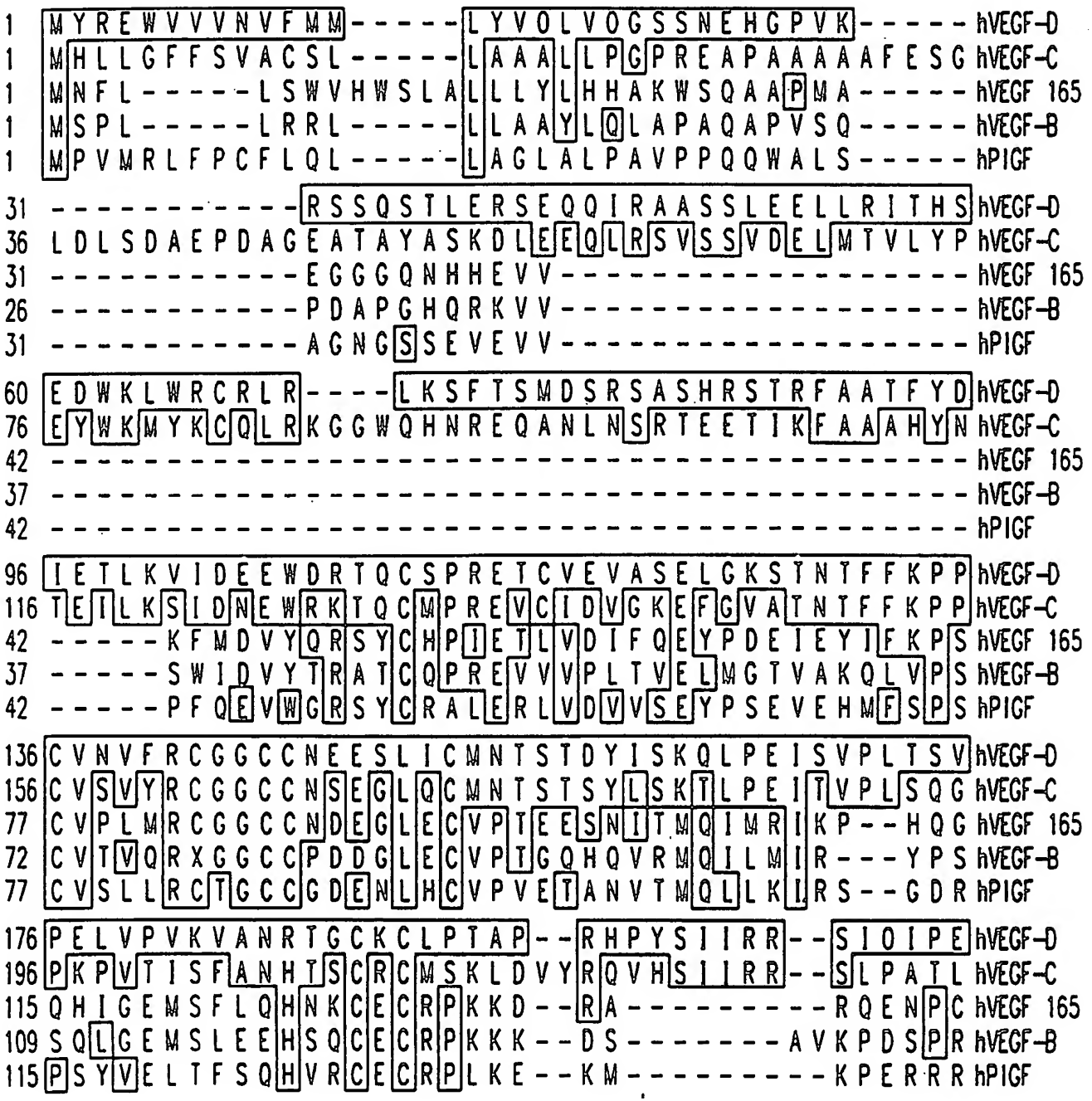

1 MYREWVVVNVFMM------LYVQLVQGSSNEHGPVK------ hVEGF-D
1 MHLLGFFSVACSL------LAAAALLPGPREAPAAAAAAFESG hVEGF-C
1 MNFL------LSWVHWSLALLLYLHHAKWSQAAPMA------ hVEGF 165
1 MSPL------LRRL------LLAAYLQLAPAQAPVSQ------ hVEGF-B
1 MPVMRLFPCFLQL------LAGLALPAVPPQQWALS------ hPIGF
31 ------------RSSQSTLERSEQQIRAASSLEELLRITHS hVEGF-D
36 LDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYP hVEGF-C
31 ------------EGGGQNHHEVV------------------- hVEGF 165
26 ------------PDAPGHQRKVV------------------- hVEGF-B
31 ------------AGNGSSEVEVV------------------- hPIGF
60 EDWKLWRCRLR----LKSFTSMDSRSASHRSTRFAATFYD hVEGF-D
76 EYWKMYKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYN hVEGF-C
42 ------------------------------------------ hVEGF 165
37 ------------------------------------------ hVEGF-B
42 ------------------------------------------ hPIGF
96 IETLKVIDEEWDRTQCSPRETCVEVASELGKSTNTFFKPP hVEGF-D
116 TEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNTFFKPP hVEGF-C
42 -----KFMDVYQRSYCHPIETLVDIFQEYPDEIEYIFKPS hVEGF 165
37 -----SWIDVYTRATCQPREVVVPLTVELMGTVAKQLVPS hVEGF-B
42 -----PFQEVWGRSYCRALERLVDVVSEYPSEVEHMFSPS hPIGF
136 CVNVFRCGGCCNEESLICMNTSTDYISKQLPEISVPLTSV hVEGF-D
156 CVSVYRCGGCCNSEGLQCMNTSTSYLSKTLPEITVPLSQG hVEGF-C
77 CVPLMRCGGCCNDEGLECVPTEESNITMQIMRIKP--HQG hVEGF 165
72 CVTVQRXGGCCPDDGLECVPTGQHQVRMQILMIR---YPS hVEGF-B
77 CVSLLRCTGCCGDENLHCVPVETANVTMQLLKIRS--GDR hPIGF
176 PELVPVKVANRTGCKCLPTAP--RHPYSIIRR--SIQIPE hVEGF-D
196 PKPVTISFANHTSCRCMSKLDVYRQVHSIIRR--SLPATL hVEGF-C
115 QHIGEMSFLQHNKCECRPKKD--RA----------RQENPC hVEGF 165
109 SQLGEMSLEEHSQCECRPKKK--DS--------AVKPDSPR hVEGF-B
115 PSYVELTFSQHVRCECRPLKE--KM----------KPERRR hPIGF

FIG. 10A

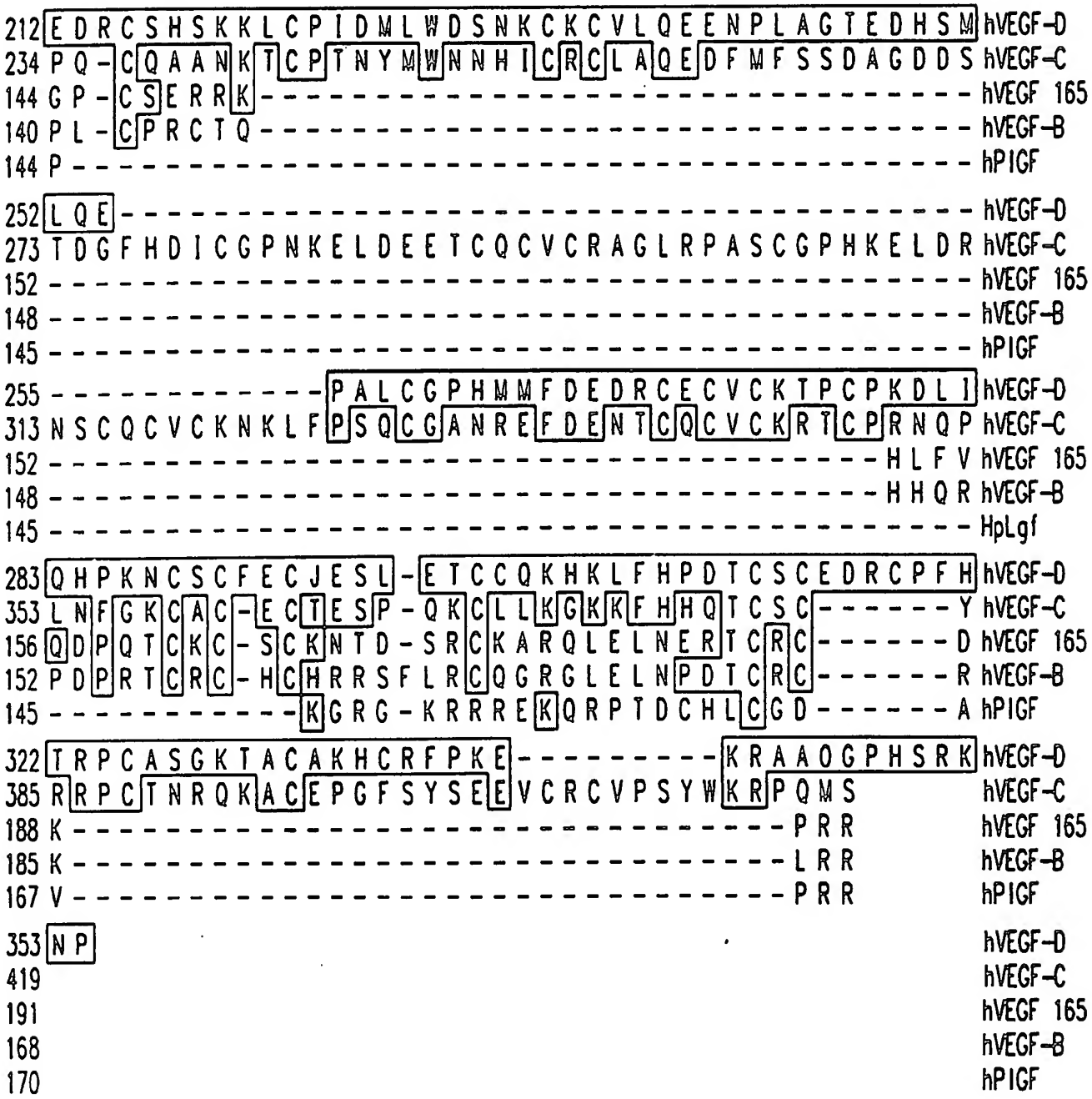
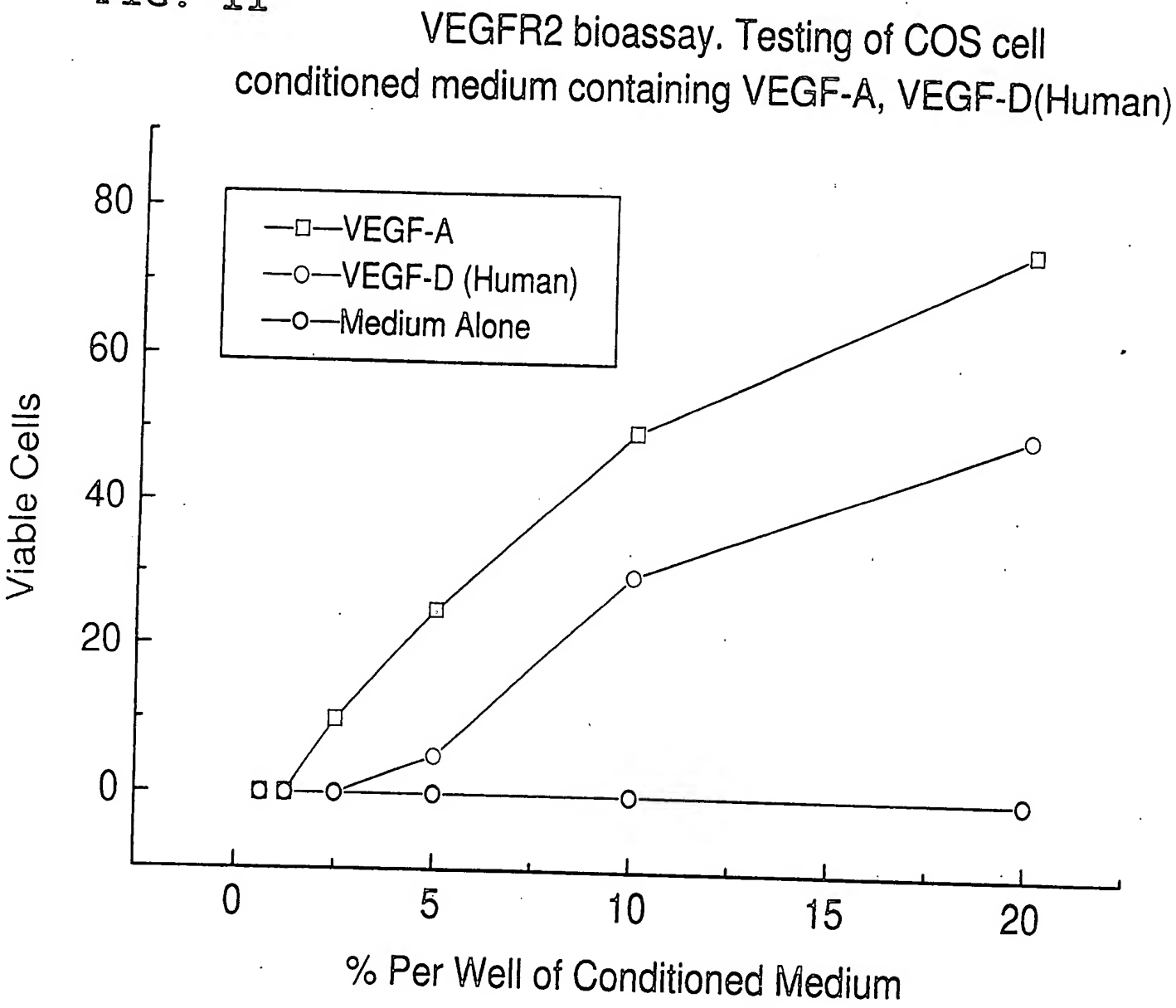

212 E D R C S H S K K L C P I D M L W D S N K C K C V L Q E E N P L A G T E D H S M hVEGF-D
234 P Q - C Q A A N K T C P T N Y M W N N H I C R C L A Q E D F M F S S D A G D D S hVEGF-C
144 G P - C S E R R K - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - hVEGF 165
140 P L - C P R C T Q - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - hVEGF-B
144 P - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - hPIGF
252 L Q E - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - hVEGF-D
273 T D G F H D I C G P N K E L D E E T C Q C V C R A G L R P A S C G P H K E L D R hVEGF-C
152 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - hVEGF 165
148 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - hVEGF-B
145 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - hPIGF
255 - - - - - - - - - - - - P A L C G P H M M F D E D R C E C V C K T P C P K D L I hVEGF-D
313 N S C Q C V C K N K L F P S Q C G A N R E F D E N T C Q C V C K R T C P R N Q P hVEGF-C
152 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - H L F V hVEGF 165
148 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - H H Q R hVEGF-B
145 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - HpLgf
283 Q H P K N C S C F E C J E S L - E T C C Q K H K L F H P D T C S C E D R C P F H hVEGF-D
353 L N F G K C A C - E C T E S P - Q K C L L K G K K F H H Q T C S C - - - - - - - Y hVEGF-C
156 Q D P Q T C K C - S C K N T D - S R C K A R Q L E L N E R T C R C - - - - - - - D hVEGF 165
152 P D P R T C R C - H C H R R S F L R C Q G R G L E L N P D T C R C - - - - - - - R hVEGF-B
145 - - - - - - - - - - - - K G R G - K R R R E K Q R P T D C H L C G D - - - - - - - A hPIGF
322 T R P C A S G K T A C A K H C R F P K E - - - - - - - - - - K R A A Q G P H S R K hVEGF-D
385 R R P C T N R Q K A C E P G F S Y S E E V C R C V P S Y W K R P Q M S hVEGF-C
188 K - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - P R R hVEGF 165
185 K - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - L R R hVEGF-B
167 V - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - P R R hPIGF
353 N P hVEGF-D
419 hVEGF-C
191 hVEGF 165
168 hVEGF-B
170 hPIGF

FIG. 10B

FIG. 11


VEGFR2 bioassay. Testing of COS cell conditioned medium containing VEGF-A, VEGF-D(Human)
VEGF-A
VEGF-D (Human)
Medium Alone
Viable Cells
80
60
40
20
0
0
5
10
15
20
% Per Well of Conditioned Medium

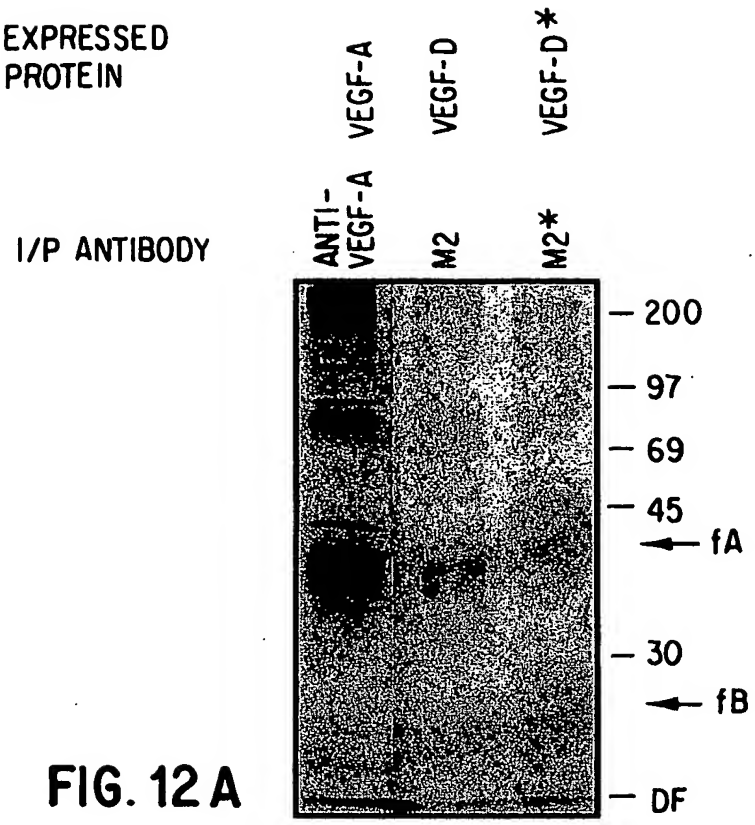



FIG. 12A

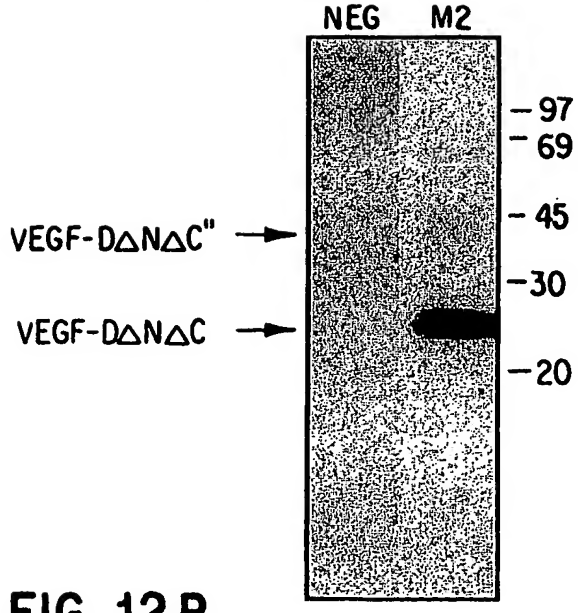
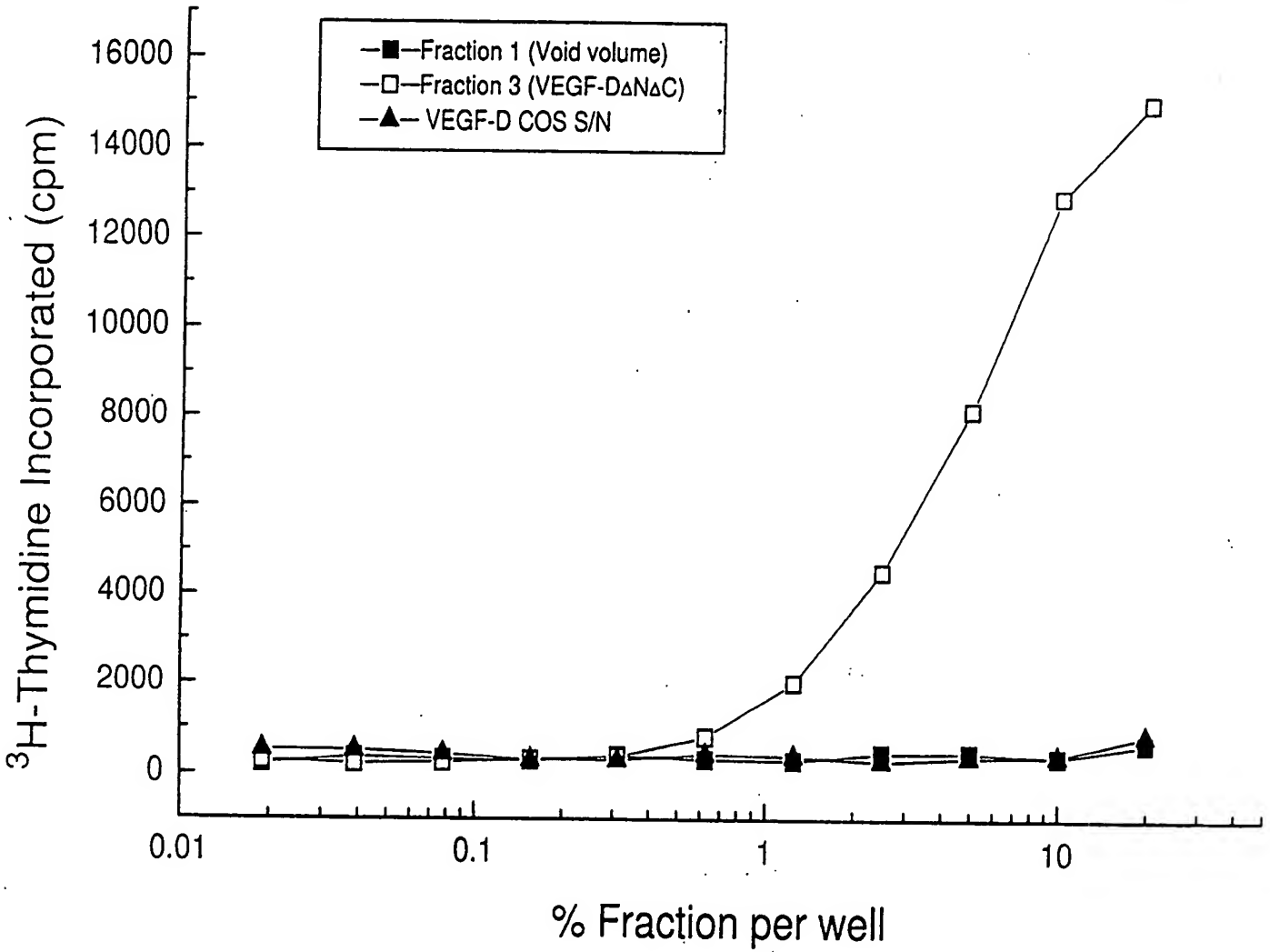



FIG. 12B

FIG. 13


—■—Fraction 1 (Void volume)
—□—Fraction 3 (VEGF-DΔNΔC)
—▲— VEGF-D COS S/N
16000
14000
12000
10000
8000
6000
4000
2000
0
$^3$H-Thymidine Incorporated (cpm)
0.01
0.1
1
10
% Fraction per well

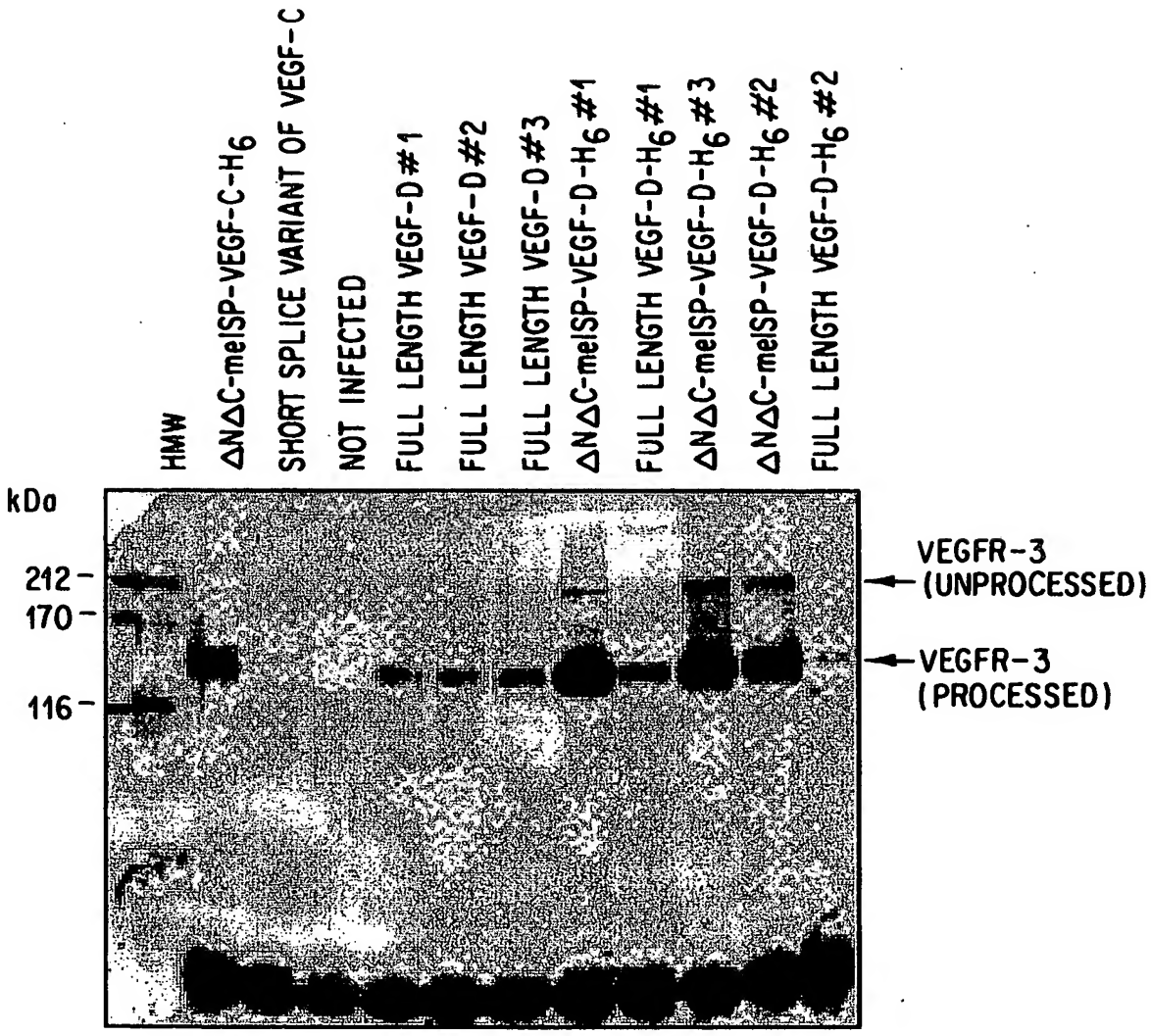

HMW
ΔNΔC-melSP-VEGF-C-H6
SHORT SPLICE VARIANT OF VEGF-C
NOT INFECTED
FULL LENGTH VEGF-D #1
FULL LENGTH VEGF-D #2
FULL LENGTH VEGF-D #3
ΔNΔC-melSP-VEGF-D-H6 #1
FULL LENGTH VEGF-D-H6 #1
ΔNΔC-melSP-VEGF-D-H6 #3
ΔNΔC-melSP-VEGF-D-H6 #2
FULL LENGTH VEGF-D-H6 #2
kDa
212
170
116
VEGFR-3 (UNPROCESSED)
VEGFR-3 (PROCESSED)

FIG. 14

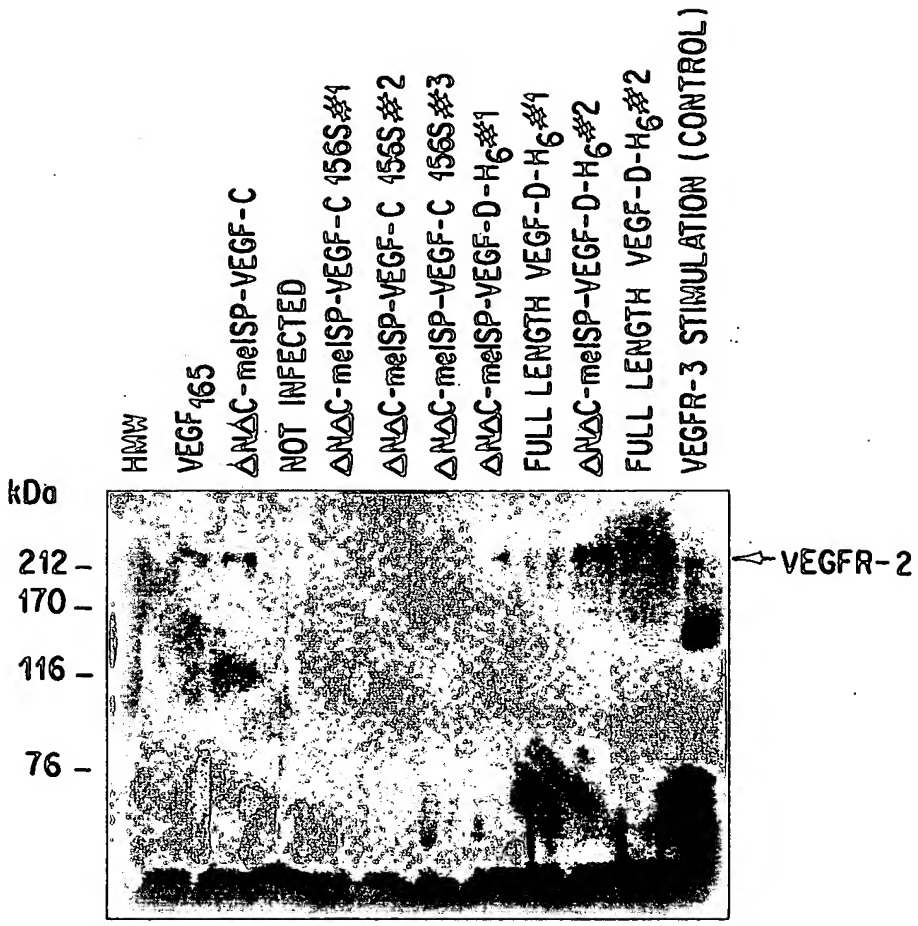
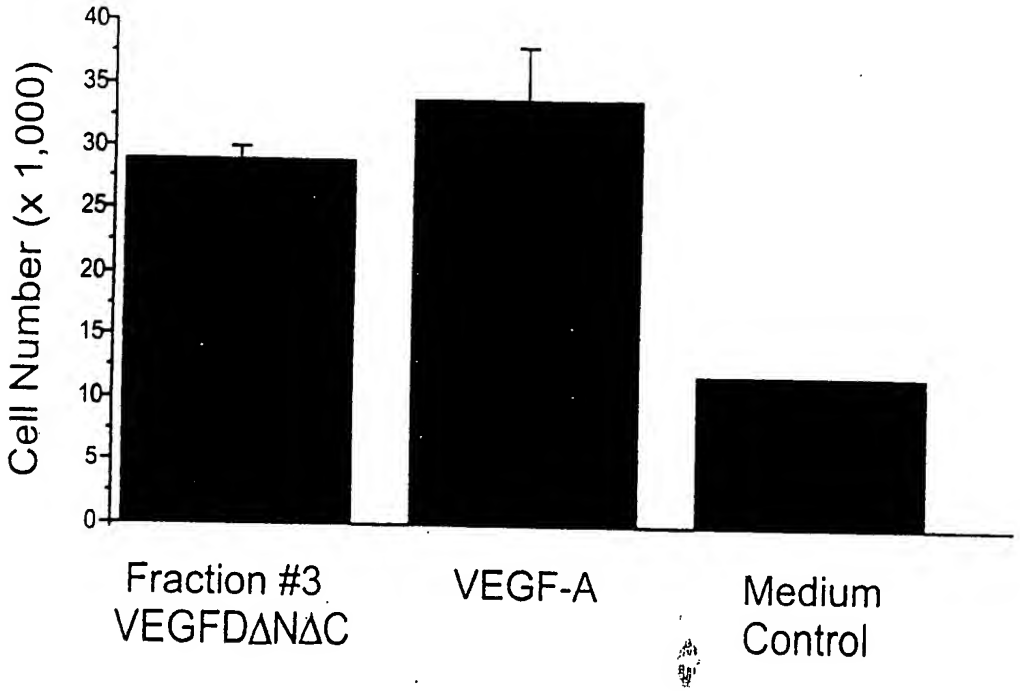

kDa
212 –
170 –
116 –
76 –
HMW
VEGF165
ΔNΔC-melSP-VEGF-C
NOT INFECTED
ΔNΔC-melSP-VEGF-C 156S#1
ΔNΔC-melSP-VEGF-C 156S#2
ΔNΔC-melSP-VEGF-C 156S#3
ΔNΔC-melSP-VEGF-D-H6#1
FULL LENGTH VEGF-D-H6#1
ΔNΔC-melSP-VEGF-D-H6#2
FULL LENGTH VEGF-D-H6#2
VEGFR-3 STIMULATION (CONTROL)
VEGFR-2

FIG. 15

FIG. 16


Cell Number (x 1,000)
40
35
30
25
20
15
10
5
0
Fraction #3
VEGFDΔNΔC
VEGF-A
Medium
Control